



#16/60

Sequence Listing

<110> Lasky, Laurence A.
Dowbenko, Donald J.

<120> Tyrosine Phosphorylated Cleavage Furrow-Associated
Proteins (PSTPIP)

<130> P1066P2

<140> US 09/068,377

<141> 1998-05-08

<150> PCT/US98/01774

<151> 1998-01-30

<150> US 08/938,830

<151> 1997-09-29

<150> US 08/798,419

<151> 1997-02-07

<160> 73

<210> 1

<211> 415

<212> PRT

<213> Mus Musculus

<400> 1

Met Met Ala Gln Leu Gln Phe Arg Asp Ala Phe Trp Cys Arg Asp
1 5 10 15

Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu
20 25 30

Asp Gly Arg Lys Met Cys Lys Asp Val Glu Glu Leu Leu Arg Gln
35 40 45

Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
50 55 60

Ala Arg Lys Ala Gly Gly Gln Thr Glu Met Asn Ser Leu Arg Thr
65 70 75

Ser Phe Asp Ser Leu Lys Gln Gln Thr Glu Asn Val Gly Ser Ala
80 85 90

His Ile Gln Leu Ala Leu Ala Leu Arg Glu Glu Leu Arg Ser Leu
95 100 105

Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Tyr Glu
110 115 120

Ala Ile Met Asp Arg Val Gln Lys Ser Lys Leu Ser Leu Tyr Lys
125 130 135

Lys Thr Met Glu Ser Lys Lys Ala Tyr Asp Gln Lys Cys Arg Asp
140 145 150

Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Val Ser Ala Asn Gly
155 160 165

His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys Ala Lys Gln Cys
170 175 180

Lys Glu Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg Gln Asn Ile
185 190 195

Glu Gln Leu Glu Arg Ala Arg Thr Glu Trp Glu Gln Glu His Arg
200 205 210

Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe Asp Arg Leu Thr
215 220 225

Ile Leu Arg Asn Ala Leu Trp Val His Cys Asn Gln Leu Ser Met
230 235 240

Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr
245 250 255

Leu Glu Gly Cys Asp Val Glu Gly Asp Ile Asn Gly Phe Ile Gln
260 265 270

Ser Lys Ser Thr Gly Arg Glu Pro Pro Ala Pro Val Pro Tyr Gln
275 280 285

Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Ile Gly Ser Pro Ser
290 295 300

Ile Gln Pro Ser Cys Gly Val Ile Lys Arg Phe Ser Gly Leu Leu
305 310 315

His Gly Ser Pro Lys Thr Thr Pro Ser Ala Pro Ala Ala Ser Thr
320 325 330

Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Leu Val Tyr Ala
335 340 345

Ser Ile Glu Val Gln Ala Thr Gln Gly Asn Leu Asn Ser Ser Ala
350 355 360

Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp
365 370 375

Glu Leu Asp Ile Ser Ala Gly Asp Ile Leu Ala Val Ile Leu Glu
380 385 390

Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly
395 400 405

Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu
410 415

<210> 2

<211> 2100

<212> DNA

<213> Mus Musculus

<400> 2

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attgctgata gctcattgtc cttcactttc actaacagta gcaacggtcc 150

gaacctcata acaactcaaa caaattctca agcgcttca caaccaattg 200

cctcctctaa cgttcatgat aacttcatga ataatgaaat cacggctagt 250

aaaattgatg atggtaataa ttcaaaacca ctgtcacctg gttggacgga 300

ccaaactgcg tataacgcgt ttggaatcac tacagggatg tttaatacca 350

ctacaatgga tgatgtatat aactatctat tcgatgatga agatacccc 400

ccaaacccaa aaaaagaggg tgggtcgacc cacgcgtccg gtccttcct 450

catttcgctg ctgattctag ccccaaacaa aacaggttga gccttttcc 500

tcctccggca gttgcctctg gcttgtggct gccttctgag cgtttcagac 550

ggcgccggct gggagtggga gggagggcct gggctagccg cgctggact 600

gggacgtgct cctggctcct ggcccatgct cagccctgct tgaagcagga 650

gtgctagcat ttgacacaac gcccttggag gatgatggcc cagctgcagt 700

tccgagatgc cttctgggtgc agggacttca cggccccacac agggtatgag 750

gtgctactgc agaggctgct ggacggcagg aagatgtgca aggatgtgga 800

ggagctgctc agacagaggg cccaggcgga ggagaggtac gggaggagc 850

tggtcagat tgcacgcaag gctggtgcc agacagagat gaattccctg 900
aggacccctt ttgactccct gaagcagcaa acagagaatg tggcgagtgc 950
acacatccag ctggccctgg ccctgcgtga ggagctgcgg agcctggagg 1000
agttccgaga gagacagaaa gagcagcggaa agaagtatga ggccatcatg 1050
gaccgtgtcc agaagagcaa gttgtcgctc tacaagaaga ccatggagtc 1100
caagaaggca tatgaccaga agtgcagggaa tgcaaatgtat gctgagcagg 1150
ccttcgagcg tgtgagtgcc aatggccacc agaagcaagt agaaaagagc 1200
cagaacaaag ccaagcagtgc caaggagtca gccacagagg cagaaagagt 1250
gtacaggcaa aatatcgaac aactggagag agcgaggacc gagtggagc 1300
aggagcaccc gactacctgt gaggcattcc agttgcagga gtttgaccgg 1350
ctcaccatcc tccgcaatgc cctgtgggtg cactgttaacc agctctccat 1400
gcagtgtgtc aaggatgtatg agctctatga ggaagtgcgg ctgacccttg 1450
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actggcagag agccccccagc tccgggtcct tatcagaact actatgacag 1550
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tgataaaagag gttctctggg ctgctacatg gaagtcccaa gaccacacct 1650
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tgagttggtc tacgcatcca tcgaagtgc a ggcgacccag gaaaccccta 1750
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tctgatgagc tggacatttc cgcgggagac atcctggcg tcatcctgg 1850
aggggaggat ggctgggtga ctgtggagcg gaacggacaa cgtggctttg 1900
tccctgggtc gtacttggag aagctctgag gaaaggctag cagtctccac 1950
atacctccgc cctgactgtg aggtcaggac ttttttttc catcaccggcc 2000
caggcctcac gggccagaa ccaagcccg gttgtctggg catggctgg 2050
gtgctggcta ctctcaataa atgtctccca gaaggaaaaaa aaaaaaaaaa 2100

<210> 3
<211> 48
<212> PRT
<213> Mus Musculus

<400> 3
Leu Tyr Asp Tyr Thr Ala Gln Asn Ser Asp Glu Leu Asp Ile Ser
1 5 10 15

Ala Gly Asp Ile Leu Ala Val Ile Leu Glu Gly Glu Asp Gly Trp
20 25 30

Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser
35 40 45

Tyr Leu Arg

<210> 4
<211> 50
<212> PRT
<213> Homo sapien

<400> 4
Leu Tyr Gln Tyr Ile Gly Gln Asp Val Asp Glu Leu Ser Phe Asn
1 5 10 15

Val Asn Glu Val Ile Glu Ile Leu Ile Glu Asp Ser Ser Gly Trp
20 25 30

Trp Lys Gly Arg Leu His Gly Gln Glu Gly Leu Phe Pro Gly Asn
35 40 45

Tyr Val Glu Lys Ile
50

<210> 5
<211> 50
<212> PRT
<213> Homo sapien

<400> 5
Leu Tyr Asp Tyr Gln Glu Lys Ser Pro Arg Glu Val Thr Met Lys
1 5 10 15

Lys Gly Asp Ile Leu Thr Leu Leu Asn Ser Thr Asn Lys Asp Trp
20 25 30

Trp Lys Val Glu Val Asn Asp Arg Gln Gly Phe Val Pro Ala Ala
35 40 45

Tyr Val Lys Lys Leu
50

<210> 6
<211> 50
<212> PRT
<213> Homo sapien

<400> 6
Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asp Ile Glu Met Val Asp Glu Gly Trp
20 25 30

Trp Arg Gly Gln Cys Arg Gly His Phe Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Lys Leu Leu
50

<210> 7
<211> 48
<212> PRT
<213> Homo sapien

<400> 7
Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser Phe Asp
1 5 10 15

Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly Trp
20 25 30

Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
35 40 45

Tyr Val Glu

<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid epitope tag

<400> 8
Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 9
cgcgatcca ccatgatggc ccagctgcag ttc 33

<210> 10
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 10
gtacgcgtcg actcaacttgt catcgtcgac cttgttagtcg agctt 45

<210> 11
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
tgcccttctc tccacagg 18

<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
ctccttgagg ttctactagt gggggctgggt gtcctg 36

<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
gcggccgac tagtatccag tctgtgctcc atctgttac 39

<210> 14
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
gcgtttggaa tcactac 17

<210> 15
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ttatagttta gcggccgctc accggtagtc ctgggctgat g 41

<210> 16
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gtacgcgtcg accgcaactt acgactacac tgcacacag 37

<210> 17
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
ctctggcgaa gaagtcc 17

<210> 18
<211> 32
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

gatcgaattc ccagaacctc aaggagaact gc 32

<210> 19

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 19

gatcctcgag ttacacccgt gtccactctg ctggagga 38

<210> 20

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic oligopeptide

<400> 20

Gly Phe Asn Leu Arg Ile Gly Arg Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ala Glu Trp Thr

20

<210> 21

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic oligopeptide

<400> 21

Gly Phe Gly Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro
1 5 10 15

Pro Ser Ala Trp

<210> 22

<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 22
Gly Phe Gly Asn Arg Cys Gly Lys Pro Lys Gly Pro Arg Asp Pro
1 5 10 15

Pro Ser Glu Trp Thr
20

<210> 23
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic oligopeptide

<400> 23
Gly Gly Val Leu Arg Ser Ile Ser Val Pro Ala Pro Pro Thr Leu
1 5 10 15

Pro Met Ala Asp Thr
20

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
gtatatgtcc tggccagccc atggggttcc cagcag 36

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
gcagggtcgac tctagattac acccgtgtcc actctg 36

<210> 26

<211> 907
<212> PRT
<213> *Saccharomyces Pombe*

<400> 26

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Ala	Leu	Met	Ser	Arg	Thr	Lys	Ser	Ser	Leu	Ser	Val	Leu	Glu	Ser
		20						25					30	
Ile	Asp	Glu	Phe	Tyr	Ala	Lys	Arg	Ala	Ser	Ile	Glu	Arg	Glu	Tyr
			35					40					45	
Ala	Ser	Lys	Leu	Gln	Glu	Leu	Ala	Ala	Ser	Ser	Ala	Asp	Ile	Pro
			50					55					60	
Glu	Val	Gly	Ser	Thr	Leu	Asn	Asn	Ile	Leu	Ser	Met	Arg	Thr	Glu
			65					70					75	
Thr	Gly	Ser	Met	Ala	Lys	Ala	His	Glu	Glu	Val	Ser	Gln	Gln	Ile
			80					85					90	
Asn	Thr	Glu	Leu	Arg	Asn	Lys	Ile	Arg	Glu	Tyr	Ile	Asp	Gln	Thr
			95					100					105	
Glu	Gln	Gln	Lys	Val	Val	Ala	Ala	Asn	Ala	Ile	Glu	Glu	Leu	Tyr
			110					115					120	
Gln	Lys	Lys	Thr	Ala	Leu	Glu	Ile	Asp	Leu	Ser	Glu	Lys	Lys	Asp
			125					130					135	
Ala	Tyr	Glu	Tyr	Ser	Cys	Asn	Lys	Leu	Asn	Ser	Tyr	Met	Arg	Gln
			140					145					150	
Thr	Lys	Lys	Met	Thr	Gly	Arg	Glu	Leu	Asp	Lys	Tyr	Asn	Leu	Lys
			155					160					165	
Ile	Arg	Gln	Ala	Ala	Leu	Ala	Val	Lys	Lys	Met	Asp	Ala	Glu	Tyr
			170					175					180	
Arg	Glu	Thr	Asn	Glu	Leu	Leu	Leu	Thr	Val	Thr	Arg	Glu	Trp	Ile
			185					190					195	
Asp	Arg	Trp	Thr	Glu	Val	Cys	Asp	Ala	Phe	Gln	His	Ile	Glu	Glu
			200					205					210	
Tyr	Arg	Leu	Glu	Phe	Leu	Lys	Thr	Asn	Met	Trp	Ala	Tyr	Ala	Asn
			215					220					225	
Ile	Ile	Ser	Thr	Ala	Cys	Val	Lys	Asp	Asp	Glu	Ser	Cys	Glu	Lys

230	235	240
Ile Arg Leu Thr Leu Glu Asn Thr Asn Ile Asp Glu Asp Ile Thr		
245	250	255
Gln Met Ile Gln Asn Glu Gly Thr Gly Thr Thr Ile Pro Pro Leu		
260	265	270
Pro Glu Phe Asn Asp Tyr Phe Lys Glu Asn Gly Leu Asn Tyr Asp		
275	280	285
Ile Asp Gln Leu Ile Ser Lys Ala Pro Ser Tyr Pro Tyr Ser Ser		
290	295	300
Ser Arg Pro Ser Ala Ser Ala Ser Leu Ala Ser Ser Pro Thr Arg		
305	310	315
Ser Ala Phe Arg Pro Lys Thr Ser Glu Thr Val Ser Ser Glu Val		
320	325	330
Val Ser Ser Pro Pro Thr Ser Pro Leu His Ser Pro Val Lys Pro		
335	340	345
Val Ser Asn Glu Gln Val Glu Gln Val Thr Glu Val Glu Leu Ser		
350	355	360
Ile Pro Val Pro Ser Ile Gln Glu Ala Glu Ser Gln Lys Pro Val		
365	370	375
Leu Thr Gly Ser Ser Met Arg Arg Pro Ser Val Thr Ser Pro Thr		
380	385	390
Phe Glu Val Ala Ala Arg Pro Leu Thr Ser Met Asp Val Arg Ser		
395	400	405
Ser His Asn Ala Glu Thr Glu Val Gln Ala Ile Pro Ala Ala Thr		
410	415	420
Asp Ile Ser Pro Glu Val Lys Glu Gly Lys Asn Ser Glu Asn Ala		
425	430	435
Ile Thr Lys Asp Asn Asp Asp Ile Ile Leu Ser Ser Gln Leu Gln		
440	445	450
Pro Thr Ala Thr Gly Ser Arg Ser Ser Arg Leu Ser Phe Ser Arg		
455	460	465
His Gly His Gly Ser Gln Thr Ser Leu Gly Ser Ile Lys Arg Lys		
470	475	480
Ser Ile Met Glu Arg Met Gly Arg Pro Thr Ser Pro Phe Met Gly		

485	490	495
Ser Ser Phe Ser Asn Met Gly Ser Arg Ser Thr Ser Pro Thr Lys		
500	505	510
Glu Gly Phe Ala Ser Asn Gln His Ala Thr Gly Ala Ser Val Gln		
515	520	525
Ser Asp Glu Leu Glu Asp Ile Asp Pro Arg Ala Asn Val Val Leu		
530	535	540
Asn Val Gly Pro Asn Met Leu Ser Val Gly Glu Ala Pro Val Glu		
545	550	555
Ser Thr Ser Lys Glu Glu Asp Lys Asp Val Pro Asp Pro Ile Ala		
560	565	570
Asn Ala Met Ala Glu Leu Ser Ser Met Arg Arg Arg Gln Ser		
575	580	585
Thr Ser Val Asp Asp Glu Ala Pro Val Ser Leu Ser Lys Thr Ser		
590	595	600
Ser Ser Thr Arg Leu Asn Gly Leu Gly Tyr His Ser Arg Asn Thr		
605	610	615
Ser Ile Ala Ser Asp Ile Asp Gly Val Pro Lys Lys Ser Thr Leu		
620	625	630
Gly Ala Pro Pro Ala Ala His Thr Ser Ala Gln Met Gln Arg Met		
635	640	645
Ser Asn Ser Phe Ala Ser Gln Thr Lys Gln Val Phe Gly Glu Gln		
650	655	660
Arg Thr Glu Asn Ser Ala Arg Glu Ser Leu Arg His Ser Arg Ser		
665	670	675
Asn Met Ser Arg Ser Pro Ser Pro Met Leu Ser Arg Arg Ser Ser		
680	685	690
Thr Leu Arg Pro Ser Phe Glu Arg Ser Ala Ser Ser Leu Ser Val		
695	700	705
Arg Gln Ser Asp Val Val Ser Pro Ala Pro Ser Thr Arg Ala Arg		
710	715	720
Gly Gln Ser Val Ser Gly Gln Gln Arg Pro Ser Ser Ser Met Ser		
725	730	735
Leu Tyr Gly Glu Tyr Asn Lys Ser Gln Pro Gln Leu Ser Met Gln		

740	745	750
Arg Ser Val Ser Pro Asn Pro Leu Gly Pro Asn Arg Arg Ser Ser		
755	760	765
Ser Val Leu Gln Ser Gln Lys Ser Thr Ser Ser Asn Thr Ser Asn		
770	775	780
Arg Asn Asn Gly Gly Tyr Ser Gly Ser Arg Pro Ser Ser Glu Met		
785	790	795
Gly His Arg Tyr Gly Ser Met Ser Gly Arg Ser Met Arg Gln Val		
800	805	810
Ser Gln Arg Ser Thr Ser Arg Ala Arg Ser Pro Glu Pro Thr Asn		
815	820	825
Arg Asn Ser Val Gln Ser Lys Asn Val Asp Pro Arg Ala Thr Phe		
830	835	840
Thr Ala Glu Gly Glu Pro Ile Leu Gly Tyr Val Ile Ala Leu Tyr		
845	850	855
Asp Tyr Gln Ala Gln Ile Pro Glu Glu Ile Ser Phe Gln Lys Gly		
860	865	870
Asp Thr Leu Met Val Leu Arg Thr Gln Glu Asp Gly Trp Trp Asp		
875	880	885
Gly Glu Ile Ile Asn Val Pro Asn Ser Lys Arg Gly Leu Phe Pro		
890	895	900
Ser Asn Phe Val Gln Thr Val		
905		

<210> 27
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Any amino acid

<400> 27
Pro-Xaa Xaa Pro
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<210> 28
<211> 1613
<212> DNA
<213> Homo sapien

<400> 28
acgatcacta tagggcgaat tgggcctcta gatgcgtgc cgagcggccg 50
ccagtgtat ggatatctgc agaattcggc ttccatccta atacgactca 100
ctatagggct cgagcggccg cccgggcagg tctagaattc agcggccgct 150
gaattctt tttccccc tcagaagctc ctctctggct cgtggctgcc 200
ttctgagtgt tgcagacggc gccggccggg aaggggggcc tgggccagcc 250
ctgccaggac tgggacgctg ctgctgacgc ctggccctcc atcaggccag 300
cctgtggcag gagagtgagc tttgccgcgg cagacgcctg aggatgatgc 350
cccagctgca gttcaaagat gccttttgt gcagggactt cacagcccac 400
acgggctacg aggtgctgct gcagcggctt ctggatggca ggaagatgtg 450
caaagacatg gaggagctac tgaggcagag ggcccaggcg gaggagcgg 500
acgggaagga gctggtgcag atcgacgga aggtaggtgg ccagacggag 550
atcaactccc tgagggcctc ctttgactcc ttgaagcagc aaatggagaa 600
tgtggcagc tcacacatcc agctggccct gaccctgcgt gaggagctgc 650
ggagtctcga ggagttcgt gagaggcaga aggagcagag gaagaagggc 700
atggctgtcc cgagacagag tgactgcatg gaagtgaagt ccccatcatg 750
ggagtatgag gccgtcatgg accgggtcca gaagagcaag ctgtcgctct 800
acaagaaggc catggagtcc aagaagacat acgagcagaa gtgccgggac 850
gcggacgacg cggagcaggc ctgcagcgc attagcgcca acggccacca 900
gaagcaggtg gagaagagtc agaacaaggc caggcagtgc aaggactcgg 950
ccaccgaggc agagcggta tacaggcaga gcattgcgc gctggagaag 1000
gtccgggctg agtgggagca ggagcacccgg accacctgtg aggcctttca 1050
gctgcaagag tttgaccggc tgaccattct ccgcaacgccc ctgtgggtgc 1100
acagtaacca gctctccatg cagtgtgtca aggatgatga gctctacgag 1150
gaagtgcggc tgacgctgga aggctgcagc atagacgccc acatcgacag 1200
tttcatccag gccaagagca cgggcacaga gccccccagg ttctctggac 1250

tgctgcacgg aagtcccaag accacttcgt cagttctgc tggctccaca 1300
gagaccctga cccccacccc cgagcgaaat gagggtgtct acacagccat 1350
cgcagtgcag gagatacagg gaaacctcggc ctcaccagcc caggactacc 1400
ggcgctcta cgattataca gcgcagaacc cagatgagct ggacctgtcc 1450
gcgggagaca tcctggaagg ggaggatggc tggggactg tggagaggaa 1500
cgggcagcgt ggcttcgtcc ctggttccta cctggagaag ctttggggaa 1550
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ccccagcact gtc 1613

<210> 29
<211> 400
<212> PRT
<213> Homo sapien

<400> 29
Met Met Pro Gln Leu Gln Phe Lys Asp Ala Phe Trp Cys Arg Asp
1 5 10 15
Phe Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu
20 25 30
Asp Gly Arg Lys Met Cys Lys Asp Met Glu Glu Leu Leu Arg Gln
35 40 45
Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile
50 55 60
Ala Arg Lys Ala Gly Gly Gln Thr Glu Ile Asn Ser Leu Arg Ala
65 70 75
Ser Phe Asp Ser Leu Lys Gln Gln Met Glu Asn Val Gly Ser Ser
80 85 90
His Ile Gln Leu Ala Leu Thr Leu Arg Glu Glu Leu Arg Ser Leu
95 100 105
Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Gly Met
110 115 120
Ala Val Pro Arg Gln Ser Asp Cys Met Glu Val Lys Ser Pro Ser
125 130 135
Trp Glu Tyr Glu Ala Val Met Asp Arg Val Gln Lys Ser Lys Leu

140	145	150
Ser Leu Tyr Lys Lys Ala Met Glu Ser Lys Lys Thr Tyr Glu Gln		
155	160	165
Lys Cys Arg Asp Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg Ile		
170	175	180
Ser Ala Asn Gly His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys		
185	190	195
Ala Arg Gln Cys Lys Asp Ser Ala Thr Glu Ala Glu Arg Val Tyr		
200	205	210
Arg Gln Ser Ile Ala Gln Leu Glu Lys Val Arg Ala Glu Trp Glu		
215	220	225
Gln Glu His Arg Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe		
230	235	240
Asp Arg Leu Thr Ile Leu Arg Asn Ala Leu Trp Val His Ser Asn		
245	250	255
Gln Leu Ser Met Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu		
260	265	270
Val Arg Leu Thr Leu Glu Gly Cys Ser Ile Asp Ala Asp Ile Asp		
275	280	285
Ser Phe Ile Gln Ala Lys Ser Thr Gly Thr Glu Pro Pro Arg Phe		
290	295	300
Ser Gly Leu Leu His Gly Ser Pro Lys Thr Thr Ser Ser Ala Ser		
305	310	315
Ala Gly Ser Thr Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu		
320	325	330
Gly Val Tyr Thr Ala Ile Ala Val Gln Glu Ile Gln Gly Asn Pro		
335	340	345
Ala Ser Pro Ala Gln Asp Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala		
350	355	360
Gln Asn Pro Asp Glu Leu Asp Leu Ser Ala Gly Asp Ile Leu Glu		
365	370	375
Gly Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly		
380	385	390
Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu		

<210> 30
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 30
cagttcgat ccatgatgct gcagaggctg ctggacggca gg 42

<210> 31
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
cagttcgat ccatgatgga gaggtacggg aaggagctgg tg 42

<210> 32
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<210> 63
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gaaggcctcg gaggttagtcc ggtgctc 27

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ctgcaggagg atccgcgggc cctttgggcc ttcc 34

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